

SEQUENCE LISTING

<110> Istituto Superiore di Sanità
National Institutes of Health

<120> COLORECTAL ANTIGEN

<130> WPP88367

<150> US 60/512,040
<151> 2003-10-15

<160> 20

<170> PatentIn version 3.3

<210> 1
<211> 1413
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (85)..(1395)

<220>
<221> misc_feature
<222> (1180)..(1240)
<223> nucleotide sequence encoding the immunogenic peptide

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Met Ala Phe Met Thr Arg Lys Leu Trp
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gac ctg gag cag cag gtg aag gcc cag act gat gag ata ctg tcc aag 159
Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu Ile Leu Ser Lys
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gat cag aag ata gcg gcc cta gag gac ctg gtg cag acc ctc cgg cca 207
Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln Thr Leu Arg Pro
30 35 40
cac cca gcc gag gca acc ctg cag cgg cag gag gaa ctg gag acg atg 255
His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu Leu Glu Thr Met
45 50 55
tgt gtg cag ctg cag cgg cag gtc agg gag atg gag cgg ttc ctc agt 303
Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu Arg Phe Leu Ser
60 65 70
gac tat ggc ctg cag tgg gtg ggc gag ccc atg gac cag gag gac tca 351
Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp Gln Glu Asp Ser
75 80 85
gag agc aag aca gtc tca gag cat ggc gag agg gac tgg atg aca gcc 399
Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp Trp Met Thr Ala
90 95 100 105
aag aag ttc tgg aag cca ggg gac tca ttg gcg ccc cct gag gtg gac 447
Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro Pro Glu Val Asp
110 115 120
ttt gac agg ctg ctg gcc agc ctg cag gat ctt agt gag ctg gtg gta 495
Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu Val Val

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tac ccc aat ggg gtc ccc ttt aag gtg agt gac ttg cgc aat cag gtc Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn Gln Val 205 210 215			735
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ggc tcc agg atg act gct gag aaa ttt ctg aac agg ctc ccc aag ttt Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro Lys Phe 250 255 260 265			879
gtg atc cgg caa ggc gag gtg att gac atc cgg ggc ccc atc agg gac Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile Arg Asp 270 275 280			927
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gtg gag acg ccc acc ttg gcc gct gag cga gag agg agc cag gag tca Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln Glu Ser 300 305 310			1023
ccc aac aca ccg gca ccc ccg ctc tcc atg ctg cgc atc aag tct gag Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys Ser Glu 315 320 325			1071
aat ggg gaa cag gcc ttc cta ctg atg atg cag cct gac aac acc att Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn Thr Ile 330 335 340 345			1119
ggg gac gtg cga gct ctg cta gcg cag gcc agg gtc atg gat gcc tct Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp Ala Ser 350 355 360			1167
gcc ttt gag atc ttc agc aca ttc ccg ccc acc ctc tac cag gac gat Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp 365 370 375			1215
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ctg cgg gca cgc cga gcc ccg aag tcc agc ctg aaa ttc agt cct ggt Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser Pro Gly 1311			

395 400 405
 ccc tgt ccc ggt ccc ggt ccc ggc ccc agt ccc ggt ccc ggt ccc ggc 1359
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 410 415 420 425

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 <213> Homo sapiens

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 35 40 45

 Gln Arg Gln Glu Glu Leu Glu Thr Met Cys Val Gln Leu Gln Arg Gln
 50 55 60

 Val Arg Glu Met Glu Arg Phe Leu Ser Asp Tyr Gly Leu Gln Trp Val
 65 70 75 80

 Gly Glu Pro Met Asp Gln Glu Asp Ser Glu Ser Lys Thr Val Ser Glu
 85 90 95

 His Gly Glu Arg Asp Trp Met Thr Ala Lys Lys Phe Trp Lys Pro Gly
 100 105 110

 Asp Ser Leu Ala Pro Pro Glu Val Asp Phe Asp Arg Leu Leu Ala Ser
 115 120 125

 Leu Gln Asp Leu Ser Glu Leu Val Val Glu Gly Asp Thr Gln Val Thr
 130 135 140

 Pro Val Pro Gly Gly Ala Arg Leu Arg Thr Leu Glu Pro Ile Pro Leu
 145 150 155 160

 Lys Leu Tyr Arg Asn Gly Ile Met Met Phe Asp Gly Pro Phe Gln Pro
 165 170 175

 Phe Tyr Asp Pro Ser Thr Gln Arg Cys Leu Arg Asp Ile Leu Asp Gly
 180 185 190

Phe Phe Pro Ser Glu Leu Gln Arg Leu Tyr Pro Asn Gly Val Pro Phe
 195 200 205

Lys Val Ser Asp Leu Arg Asn Gln Val Tyr Leu Glu Asp Gly Leu Asp
 210 215 220

Pro Phe Pro Gly Glu Gly Arg Val Val Gly Arg Gln Arg Met His Lys
 225 230 235 240

Ala Leu Asp Arg Val Glu Glu His Pro Gly Ser Arg Met Thr Ala Glu
 245 250 255

Lys Phe Leu Asn Arg Leu Pro Lys Phe Val Ile Arg Gln Gly Glu Val
 260 265 270

Ile Asp Ile Arg Gly Pro Ile Arg Asp Thr Leu Gln Asn Cys Cys Pro
 275 280 285

Leu Pro Ala Arg Ile Gln Glu Ile Val Val Glu Thr Pro Thr Leu Ala
 290 295 300

Ala Glu Arg Glu Arg Ser Gln Glu Ser Pro Asn Thr Pro Ala Pro Pro
 305 310 315 320

Leu Ser Met Leu Arg Ile Lys Ser Glu Asn Gly Glu Gln Ala Phe Leu
 325 330 335

Leu Met Met Gln Pro Asp Asn Thr Ile Gly Asp Val Arg Ala Leu Leu
 340 345 350

Ala Gln Ala Arg Val Met Asp Ala Ser Ala Phe Glu Ile Phe Ser Thr
 355 360 365

Phe Pro Pro Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala
 370 375 380

Gly Leu Val Pro Lys Ala Ala Leu Leu Leu Arg Ala Arg Arg Ala Pro
 385 390 395 400

Lys Ser Ser Leu Lys Phe Ser Pro Gly Pro Cys Pro Gly Pro Gly Pro
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Ser Pro Ser Pro Gln
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 <213> Homo sapiens

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Gln Ala Ala Gly
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Thr Ala Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro Pro Glu
 35 40 45

Val Asp Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu
 50 55 60

Val Val Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly Ala Arg
 65 70 75 80

Leu Arg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn Gly Ile
 85 90 95

Met Met Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser Thr Gln
 100 105 110

Arg Cys Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu Leu Gln
 115 120 125

Arg Leu Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn
 130 135 140

Gln Val Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu Gly Arg
 145 150 155 160

Val Val Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val Glu Glu
 165 170 175

His Pro Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro
 180 185 190

Lys Phe Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile
 195 200 205

Arg Asp Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile Gln Glu
 210 215 220

Ile Val Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln
 225 230 235 240

Glu Ser Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys
 245 250 255

Ser Glu Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn
 260 265 270

Thr Ile Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp
 275 280 285

Ala Ser Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln
 290 295 300

Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala
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Pro Gly Pro Cys Pro Gly Pro
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<210> 10
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 <212> PRT
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<400> 10

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 35 40 45
 Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser Pro Gly
 50 55 60
 Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly Pro Gly Pro Gly
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 Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln
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 <213> ARTIFICIAL

<220>
 <223> PCR primer sequence

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 <211> 18
 <212> DNA
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<220>
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<400> 14
 ccttgaatgt ggtcatct 18

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<220>
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<400> 15
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23

<210> 16
<211> 20
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<220>
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<210> 17
<211> 20
<212> PRT
<213> Homo sapiens

<400> 17

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Gln Ala Ala Gly
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<210> 18
<211> 20
<212> PRT
<213> Homo sapiens

<400> 18

Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val
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Pro Lys Ala Ala
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<212> DNA
<213> Homo sapiens

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aggagcaggc agataacaga aacttccaga aacctctgtg gagacagtgg aagaggcaaa 180
agggagttcc tgacagctgg attctagaag tagaactatg agctcacctt tggcctccct 240

tagcaagacc cgaaaagtgc ccctgccctc ggagcctatg aatcctggga ggcgaggaat 300
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<211> 512

<212> PRT

<213> Homo sapiens

<400> 20

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 35 40 45

Lys Ile Ser Val Pro Ser Cys Tyr Gly Gly Ile Gly Ala Pro Val Ser
 50 55 60

Arg Gln Val Pro Ala Ser His Asp Ser Glu Leu Met Ala Phe Met Thr
 65 70 75 80

Arg Lys Leu Trp Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu
 85 90 95

Ile Leu Ser Lys Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln
 100 105 110

Thr Leu Arg Pro His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu
 115 120 125

Leu Glu Thr Met Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu
 130 135 140

Arg Phe Leu Ser Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp
 145 150 155 160

Gln Glu Asp Ser Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp
 165 170 175

Trp Met Thr Ala Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro
 180 185 190

Pro Glu Val Asp Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser
 195 200 205

Glu Leu Val Val Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly
 210 215 220

Ala Arg Leu Arg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn
 225 230 235 240

Gly Ile Met Met Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser
 245 250 255

Thr Gln Arg Cys Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu
 260 265 270

Leu Gln Arg Leu Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu
 275 280 285

Arg Asn Gln Val Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu
 290 295 300

Gly Arg Val Val Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val
305 310 315 320

Glu Glu His Pro Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg
325 330 335

Leu Pro Lys Phe Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly
340 345 350

Pro Ile Arg Asp Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile
355 360 365

Gln Glu Ile Val Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg
370 375 380

Ser Gln Glu Ser Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg
385 390 395 400

Ile Lys Ser Glu Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro
405 410 415

Asp Asn Thr Ile Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val
420 425 430

Met Asp Ala Ser Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu
435 440 445

Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys
450 455 460

Ala Ala Leu Leu Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys
465 470 475 480

Phe Ser Pro Gly Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly
485 490 495

Pro Gly Pro Gly Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln
500 505 510